

#6

OIKE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/784,911

DATE: 10/01/2001

TIME: 10:21:25

Input Set : A:\13406.asc

Output Set: N:\CRF3\10012001\I784911.raw

3 <110> APPLICANT: Harrison, Leonard C.  
4 Jiang, Fang-Xu  
5 Stanley, Edouard Guy  
6 Gonez, Leonel Jorge  
8 <120> TITLE OF INVENTION: Pancreatic islet cell growth factors  
10 <130> FILE REFERENCE: Davies Collison Cave  
12 <140> CURRENT APPLICATION NUMBER: 09/784,911  
C--> 13 <141> CURRENT FILING DATE: 2001-09-17  
15 <160> NUMBER OF SEQ ID NOS: 30  
17 <170> SOFTWARE: PatentIn version 2.1  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 1260  
21 <212> TYPE: DNA  
22 <213> ORGANISM: mouse  
24 <220> FEATURE:  
25 <221> NAME/KEY: CDS  
26 <222> LOCATION: (1)..(1260)  
28 <220> FEATURE:  
29 <221> NAME/KEY: UNSURE  
30 <222> LOCATION: (186)  
31 <223> OTHER INFORMATION: Xaa at position 186 is Tyr or His  
33 <400> SEQUENCE: 1

34	atg gcg cgc ctg atg att cct ggt aac cga atg ctg atg gtc gtt tta	48
35	Met Ala Arg Leu Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu	
36	1 5 10 15	
38	tta tgc caa gtc ctg cta gga ggc gcg agc cat gct agt ttg ata cct	96
39	Leu Cys Gln Val Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro	
40	20 25 30	
42	gag acc ggg aag aaa aaa gtc gcc gag att cag ggc cac gcg gga gga	144
43	Glu Thr Gly Lys Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly	
44	35 40 45	
46	cgc cgc tca ggg cag agc cat gag ctc ctg cgg gac ttc gag gcg aca	192
47	Arg Arg Ser Gly Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr	
48	50 55 60	
50	ctt cta cag atg ttt ggg ctg cgc cgc cgt ccg cag cct agc aag agc	240
51	Leu Leu Gln Met Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser	
52	65 70 75 80	
54	gcc gtc att ccg gat tac atg agg gat ctt tac cgg ctc cag tct ggg	288
55	Ala Val Ile Pro Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly	
56	85 90 95	
58	gag gag gag gag gaa gag cag agc cag gga acc ggg ctt gag tac ccg	336
59	Glu Glu Glu Glu Glu Glu Gln Ser Gln Gly Thr Gly Leu Glu Tyr Pro	
60	100 105 110	
62	gag cgt ccc gcc agc cga gcc aac act gtg agg agt ttc cat cac gaa	384
63	Glu Arg Pro Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His His Glu	
64	115 120 125	
66	gaa cat ctg gag aac atc cca ggg acc agt gag agc tct gct ttt cgt	432

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67  Glu His Leu Glu Asn Ile Pro Gly Thr Ser Glu Ser Ser Ala Phe Arg
68      130                      135                      140
70  ttc ctc ttc aac ctc agc agc atc cca gaa aat gag gtg atc tcc tcg      480
71  Phe Leu Phe Asn Leu Ser Ser Ile Pro Glu Asn Glu Val Ile Ser Ser
72  145                      150                      155                      160
74  gca gag ctc cgg ctc ttt cgg gag cag gtg gac cag ggc cct gac tgg      528
76  Ala Glu Leu Arg Leu Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp
77      165                      170                      175
79  gaa cag ggc ttc cac cgt ata aac att yat gag gtt atg aag ccc cca      576
W--> 80  Glu Gln Gly Phe His Arg Ile Asn Ile Xaa Glu Val Met Lys Pro Pro
81      180                      185                      190
83  gca gaa atg gtt cct gga cac ctc atc aca cga cta ctg gac acc aga      624
84  Ala Glu Met Val Pro Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg
85      195                      200                      205
87  cta gtc cat cac aat gtg aca cgg tgg gaa act ttc gat gtg agc cct      672
88  Leu Val His His Asn Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro
89      210                      215                      220
91  gca gtc ctt cgc tgg acc cgg gaa aag caa ccc aat tat ggg ctg gcc      720
92  Ala Val Leu Arg Trp Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala
93  225                      230                      235                      240
95  att gag gtg act cac ctc cac cag aca cgg acc cac cag ggc cag cat      768
96  Ile Glu Val Thr His Leu His Gln Thr Arg Thr His Gln Gly Gln His
97      245                      250                      255
99  gtc aga atc agc cga tcg tta cct caa ggg agt gga gat tgg gcc caa      816
100  Val Arg Ile Ser Arg Ser Leu Pro Gln Gly Ser Gly Asp Trp Ala Gln
101      260                      265                      270
103  ctc cgg ccc ctc ctg gtc act ttt ggc cat gat ggc cgg ggc cat acc      864
104  Leu Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Arg Gly His Thr
105      275                      280                      285
107  ttg acc cgc agg agg gcc aaa cgt agt ccc aag acg cgc cag gag gag      912
108  Leu Thr Arg Arg Arg Ala Lys Arg Ser Pro Lys Thr Arg Gln Glu Glu
109      290                      295                      300
111  gaa tac atg ccc atg gag acg cgt agg aag aag aat aag aac tgc cgt      960
112  Glu Tyr Met Pro Met Glu Thr Arg Arg Lys Lys Asn Lys Asn Cys Arg
113  305                      310                      315                      320
115  cgc cat tca cta tac gtg gac ttc agt gac gtg ggc tgg aat gat tgg      1008
116  Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp
117      325                      330                      335
119  att gtg gcc cca ccc ggc tac cag gcc ttc tac tgc cat ggg gac tgt      1056
120  Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp Cys
121      340                      345                      350
123  ccc ttt cca ctg gct gat cac ctc aac tca acc aac cat gcc att gtg      1104
125  Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val
126      355                      360                      365
128  cag acc cta gtc aac tct gtt aat tct agt atc cct aag gcc tgt tgt      1152
129  Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala Cys Cys
130      370                      375                      380
132  gtc ccc act gaa ctg agt gcc att tcc atg ttg tac ctg gat gag tat      1200
133  Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Tyr

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Input Set : A:\13406.asc

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```

134      385              390              395              400
136      gac aag gtg gtg ttg aaa aat tat cag gag atg gtg gta gag ggg tgt      1248
137      Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu Gly Cys
138              405              410              415
140      gga tgc cgc tga      1260
141      Gly Cys Arg
145 <210> SEQ ID NO: 2
146 <211> LENGTH: 419
147 <212> TYPE: PRT
148 <213> ORGANISM: mouse
150 <220> FEATURE:
151 <221> NAME/KEY: UNSURE
152 <222> LOCATION: (186)
153 <223> OTHER INFORMATION: Xaa at position 186 is Tyr or His
155 <400> SEQUENCE: 2
157      Met Ala Arg Leu Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu
158      1              5              10              15
161      Leu Cys Gln Val Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro
162              20              25              30
165      Glu Thr Gly Lys Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly
166              35              40              45
169      Arg Arg Ser Gly Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr
170              50              55              60
173      Leu Leu Gln Met Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser
174      65              70              75              80
177      Ala Val Ile Pro Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly
178              85              90              95
181      Glu Glu Glu Glu Glu Glu Gln Ser Gln Gly Thr Gly Leu Glu Tyr Pro
182              100              105              110
185      Glu Arg Pro Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His His Glu
186              115              120              125
189      Glu His Leu Glu Asn Ile Pro Gly Thr Ser Glu Ser Ser Ala Phe Arg
190              130              135              140
193      Phe Leu Phe Asn Leu Ser Ser Ile Pro Glu Asn Glu Val Ile Ser Ser
194      145              150              155              160
196      Ala Glu Leu Arg Leu Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp
197              165              170              175
W--> 199      Glu Gln Gly Phe His Arg Ile Asn Ile Xaa Glu Val Met Lys Pro Pro
200              180              185              190
202      Ala Glu Met Val Pro Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg
203              195              200              205
206      Leu Val His His Asn Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro
207      210              215              220
209      Ala Val Leu Arg Trp Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala
210      225              230              235              240
212      Ile Glu Val Thr His Leu His Gln Thr Arg Thr His Gln Gly Gln His
213              245              250              255
215      Val Arg Ile Ser Arg Ser Leu Pro Gln Gly Ser Gly Asp Trp Ala Gln
216              260              265              270

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TIME: 10:21:25

Input Set : A:\13406.asc

Output Set: N:\CRF3\10012001\I784911.raw

```

218  Leu Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Arg Gly His Thr
219              275              280              285
221  Leu Thr Arg Arg Arg Ala Lys Arg Ser Pro Lys Thr Arg Gln Glu Glu
222              290              295              300
224  Glu Tyr Met Pro Met Glu Thr Arg Arg Lys Lys Asn Lys Asn Cys Arg
225  305              310              315              320
227  Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp
228              325              330              335
230  Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp Cys
231              340              345              350
233  Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val
234              355              360              365
236  Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala Cys Cys
237              370              375              380
239  Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Tyr
240  385              390              395              400
242  Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu Gly Cys
243              405              410              415
245  Gly Cys Arg
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 1362
250 <212> TYPE: DNA
251 <213> ORGANISM: mouse
253 <220> FEATURE:
254 <221> NAME/KEY: CDS
255 <222> LOCATION: (1)..(1311)
257 <220> FEATURE:
258 <221> NAME/KEY: UNSURE
259 <222> LOCATION: (186)
260 <223> OTHER INFORMATION: Xaa at position 186 is Tyr or His
262 <400> SEQUENCE: 3
263  atg gcg cgc ctg atg att cct ggt aac cga atg ctg atg gtc gtt tta      48
264  Met Ala Arg Leu Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu
265  1              5              10              15
267  tta tgc caa gtc ctg cta gga ggc gcg agc cat gct agt ttg ata cct      96
268  Leu Cys Gln Val Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro
269              20              25              30
271  gag acc ggg aag aaa aaa gtc gcc gag att cag ggc cac gcg gga gga      144
272  Glu Thr Gly Lys Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly
273              35              40              45
275  cgc cgc tca ggg cag agc cat gag ctc ctg cgg gac ttc gag gcg aca      192
276  Arg Arg Ser Gly Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr
277  50              55              60
279  ctt cta cag atg ttt ggg ctg cgc cgc cgt ccg cag cct agc aag agc      240
280  Leu Leu Gln Met Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser
281  65              70              75              80
283  gcc gtc att ccg gat tac atg agg gat ctt tac cgg ctc cag tct ggg      288
284  Ala Val Ile Pro Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly
285              85              90              95

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Input Set : A:\13406.asc

Output Set: N:\CRF3\10012001\I784911.raw

287	gag gag gag gag gaa gag cag agc cag gga acc ggg ctt gag tac ccg	336
288	Glu Glu Glu Glu Glu Glu Gln Ser Gln Gly Thr Gly Leu Glu Tyr Pro	
289	100 105 110	
291	gag cgt ccc gcc agc cga gcc aac act gtg agg agt ttc cat cac gaa	384
292	Glu Arg Pro Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His His Glu	
293	115 120 125	
295	gaa cat ctg gag aac atc cca ggg acc agt gag agc tct gct ttt cgt	432
296	Glu His Leu Glu Asn Ile Pro Gly Thr Ser Glu Ser Ser Ala Phe Arg	
297	130 135 140	
299	ttc ctc ttc aac ctc agc agc atc cca gaa aat gag gtg atc tcc tcg	480
300	Phe Leu Phe Asn Leu Ser Ser Ile Pro Glu Asn Glu Val Ile Ser Ser	
301	145 150 155 160	
303	gca gag ctc cgg ctc ttt cgg gag cag gtg gac cag ggc cct gac tgg	528
304	Ala Glu Leu Arg Leu Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp	
305	165 170 175	
307	gaa cag ggc ttc cac cgt ata aac att yat gag gtt atg aag ccc cca	576
W--> 308	Glu Gln Gly Phe His Arg Ile Asn Ile Xaa Glu Val Met Lys Pro Pro	
309	180 185 190	
311	gca gaa atg gtt cct gga cac ctc atc aca cga cta ctg gac acc aga	624
312	Ala Glu Met Val Pro Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg	
313	195 200 205	
315	cta gtc cat cac aat gtg aca cgg tgg gaa act ttc gat gtg agc cct	672
316	Leu Val His His Asn Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro	
317	210 215 220	
319	gca gtc ctt cgc tgg acc cgg gaa aag caa ccc aat tat ggg ctg gcc	720
320	Ala Val Leu Arg Trp Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala	
321	225 230 235 240	
323	att gag gtg act cac ctc cac cag aca cgg acc cac cag ggc cag cat	768
324	Ile Glu Val Thr His Leu His Gln Thr Arg Thr His Gln Gly Gln His	
325	245 250 255	
327	gtc aga atc agc cga tcg tta cct caa ggg agt gga gat tgg gcc caa	816
329	Val Arg Ile Ser Arg Ser Leu Pro Gln Gly Ser Gly Asp Trp Ala Gln	
330	260 265 270	
332	ctc cgg ccc ctc ctg gtc act ttt ggc cat gat ggc cgg ggc cat acc	864
333	Leu Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Arg Gly His Thr	
334	275 280 285	
336	ttg acc cgc agg agg gcc aaa cgt agt ccc aag acg cgc cag gag gag	912
337	Leu Thr Arg Arg Arg Ala Lys Arg Ser Pro Lys Thr Arg Gln Glu Glu	
338	290 295 300	
340	gaa tac atg ccc atg gag acg cgt acc cag tcg cag gac gtg tcc cgg	960
341	Glu Tyr Met Pro Met Glu Thr Arg Thr Gln Ser Gln Asp Val Ser Arg	
342	305 310 315 320	
344	ggc tcc ggt tct tca gac tac aac ggc agt gag tta aaa aca gct tgc	1008
345	Gly Ser Gly Ser Ser Asp Tyr Asn Gly Ser Glu Leu Lys Thr Ala Cys	
346	325 330 335	
348	aag aag cat gag ctc tat gtg agc ttc cag gac ctg gga tgg cag gac	1056
349	Lys Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp	
350	340 345 350	
352	tgg atc att gca ccc aaa ggc tac gct gcc aac tac tgt gat gga gag	1104

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

DATE: 10/01/2001

PATENT APPLICATION: US/09/784,911

TIME: 10:21:26

Input Set : A:\13406.asc

Output Set: N:\CRF3\10012001\I784911.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6